



# **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/8/9,669C

Art Unit / Team No. :

164,4

Date Processed by STIC:

6/19/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

M. Lubet

1644

PAGE:-1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999  
TIME: 16:48:42

INPUT SET: S32279.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply  
Corrected Diskette Needed

SEQUENCE LISTING

1  
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(1) General Information:

(i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry;  
Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;  
Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

(ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
Rejection Antigens and Uses Thereof

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fulbright & Jaworski LLP
- (B) STREET: 666 Fifth Avenue
- (C) CITY: New York City
- (D) STATE: New York
- (F) ZIP: 10103

(E) COUNTRY: USA

add the mandatory  
subheading and response

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
- (B) COMPUTER: IBM
- (C) OPERATING SYSTEM: PC-DOS
- (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/819,669
- (B) FILING DATE: 17-March-1997
- (C) CLASSIFICATION: 435

--> OK

(vii) PRIOR APPLIATION DATA:

- (A) APPLICATION NUMBER: 08/142,368
- (B) FILING DATE: 02-MAY-1994

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US92/04354
- (B) FILING DATE: 22-MAY-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/807,043
- (B) FILING DATE: 12-DECEMBER-1991

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/764,364

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:42

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46 (B) FILING DATE: 23-SEPTEMBER-1991  
47  
48 (vii) PRIOR APPLICATION DATA:  
49 (A) APPLICATION NUMBER: 07/728,838  
50 (b) FILING DATE: 9-JULY-1991  
51  
52 (vii) PRIOR APPLICATION DATA:  
53 (A) APPLICATION NUMBER: 07/705,702  
54 (B) FILING DATE: 23-May-1991  
55  
56 (viii) ATTORNEY/AGENT INFORMATION:  
57 (A) NAME: Hanson, Norman D.  
58 (B) REGISTRATION NUMBER: 30,946  
59 (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US  
60  
61 (ix) TELECOMMUNICATION INFORMATION:  
62 (A) TELEPHONE: (212)318-3168  
63 (B) TELEFAX: (212)752-5958  
64  
65  
66

## ERRORED SEQUENCES FOLLOW:

67 (2) INFORMATION FOR SEQ ID NO: 1:  
68 (i) SEQUENCE CHARACTERISTICS:  
69 (A) LENGTH: 462 base pairs  
70 (B) TYPE: nucleic acid  
71 (D) TOPOLOGY: linear  
72 (ii) MOLECULE TYPE: genomic DNA  
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
74  
75  
76  
77  
78 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60  
79 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCAATCCCT CAGCCAATGA GCTTACTGTT 120  
80 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGTGCA AGTTCCGCCT ACAGCTCTAG 180  
81 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240  
82 CCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300  
83 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT 360  
84 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420  
85 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTGTG CC 462  
86  
87  
88  
89

*insert the MANATORY subheading  
and the response for all  
nucleic acid  
sequences  
(global error)*

90 (2) INFORMATION FOR SEQ ID NO: 2:  
91 (i) SEQUENCE CHARACTERISTICS:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999  
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92 (A) LENGTH: 675 base pairs  
93 (B) TYPE: nucleic acid  
94 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

--> 96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

*same over (STRANDNESS)*

99	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT	48
100	Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly	
101	5 10 15	
102	GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA	96
103	Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu	
104	20 25 30	
105	GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA	144
106	Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr	
107	35 40 45	
108	AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG	192
109	Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln	
110	50 55 60	
111	TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC	240
112	Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser	
113	65 70 75 80	
114	TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC	288
115	Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr	
116	85 90 95	
117	GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	336
118	Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp	
119	100 105 110	
120	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG	384
121	Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu	
122	115 120 125	
123	GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432
124	Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met	
125	130 135 140	
126	GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480
127	Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys	
128	145 150 155 160	
129	AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528
130	Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe	
131	165 170 175	
132	CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT	576
133	Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys	
134	180 185 190	
135	GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG	624
136	Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu	
137	195 200 210	
138	GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	672
139	Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro	
140	220 225 230 235	
141		
142	TAG	675
143		
144		

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PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
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146 (2) INFORMATION FOR SEQ ID NO: 3:  
147 (i) SEQUENCE CHARACTERISTICS:  
148 (A) LENGTH: 228 base pairs  
149 (B) TYPE: nucleic acid  
150 (D) TOPOLOGY: linear  
151 (ii) MOLECULE TYPE: genomic DNA  
--> 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
153  
154  
155  
156 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTTT 60  
157 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120  
158 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC 180  
159 ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228  
160  
161

162 (2) INFORMATION FOR SEQ ID NO: 4:  
163 (i) SEQUENCE CHARACTERISTICS:  
164 (A) LENGTH: 1365 base pairs  
165 (B) TYPE: nucleic acid  
166 (D) TOPOLOGY: linear  
167 (ii) MOLECULE TYPE: genomic DNA  
--> 168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
169  
170  
171 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50  
172 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100  
173 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTGTGAGC CTTGGGTAGG 150  
174 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200  
175 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250  
176 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300  
177 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCG 350  
178 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTGAAG AAGTAAGCCG 400  
179 CTAGCTTGCG ACTCTACTCT TATCTTAAC TAGCTCGGCT TCCTGCTGGT 450  
180 ACCCTTTGTG CC 462  
181 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504  
182 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546  
183 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588  
184 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630  
185 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672  
186 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714  
187 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756  
188 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798  
189 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840  
190 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882  
191 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924  
192 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966  
193 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008  
194 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050  
195 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:43

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196	GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
197	TAG	1137
198	GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
199	TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
200	ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
201	CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
202	GTTAAAAATA AAAGTTTGAC TTGCATAC	1365
203		
204		
205		

206 (2) INFORMATION FOR SEQ ID NO: 5:  
207 (i) SEQUENCE CHARACTERISTICS:  
208 (A) LENGTH: 4698 base pairs  
209 (B) TYPE: nucleic acid  
210 (D) TOPOLOGY: linear  
211 (ii) MOLECULE TYPE: genomic DNA  
212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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213		
214	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
215	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
216	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
217	AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT	200
218	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCCCTCA	250
219	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
220	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG	350
221	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
222	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
223	ACCCTTTGTG CC	462
224	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
225	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
226	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
227	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
228	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
229	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
230	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
231	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
232	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
233	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
234	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
235	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
236	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
237	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
238	CCCCACTCCT TGCTCCGCTC TCTTTCTTTT TCCCACCTTG CCTCTGGAGC	1116
239	TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
240	TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC	1216
241	TTCAGGCTTC CCCATTGCT CCTCTCCCGA AACCTCCCC TTCTGTTC	1266
242	CCTTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
243	TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTTGCA CCTTTTCTTT	1366
244	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT	1416
245	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG	1466
246	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT	1516
247	CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/819,669C

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248	TTGGTTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCCTGGCAC	1616
249	TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666
250	CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
251	GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
252	AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCCTG	1816
253	TTCCCTTCCG	GCACCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
254	CCTCCCCCTC	TTTGCTCGAC	TTTTCAGCAG	CTTACCTCTC	CCTGCTTTCT	1916
255	GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966
256	AGCTCACCTT	TTTGTTTGT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
257	TTTTTTTTTT	GCACCTTGT	TTCCAAGATC	CCCCTCCCCC	TCCGGCTTCC	2066
258	CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCCC	TCGCTGGCTC	CCCCTCCCTT	2116
259	TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
260	CTTTTCTAGA	CTCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
261	CCTGACCCTG	CTCCCCCTCC	CCTCCAGCT	CCCCCTCTT	TTCCACCTC	2266
262	CCTTCTCTCA	GCCTGTCAAC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCCT	2316
263	TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
264	GACTTCTCT	CCAGCCGCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
265	CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCT	2466
266	ATGTGTCTCT	CTTCCCTATCT	ATCCCTTCCT	TTCTGTCCCC	TCTCCTCTGT	2516
267	CCATCACCTC	TCTCCTCCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566
268	CCTGCTTCTT	TACCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616
269	TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
270	ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
271	TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATAG	CCCTCTACTC	2766
272	TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCCTT	CCACCCTGCC	2816
273	CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
274	ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAAA	ATCAGCAGGA	2916
275	AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
276	AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAAGTGA	TGGTGAAGTT	3016
277	CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
278	CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
279	GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
280	TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
281	TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCATATGAA	GTTCTTTTTA	3266
282	GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTCTT	3316
283	TTGCTAAAAT	ATTCTTCTC	ACATATTCAT	ATTCTCCAG		3355
284	GT GTT CCT	GGC CAT CAT	TTA AGG AAG	AAT GAA GTG	AAG TGT	3396
285	AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT TTC CTG	GTG TCT	3438
286	ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG TGT AGG	TGT GAA	3480
287	AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG GAA GAA	GAA GAA	3522
288	GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA AAC CCG	GAT GGC	3564
289	TTC TCA CCT	TAG				3576
290	GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCCTAACA	TATGCCTGTA	3626
291	GCTAAGAGCA	TCTTTTTTAAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
292	TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
293	CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
294	GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
295	GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
296	TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
297	TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAAATAT	TATTTTGTCTG	3976
298	TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTTAAAGAG	ATGAAAATCT	4026
299	CTTAAATTTT	CCTTCATCTT	TAATTTTCCT	TAACTTTAGT	TTTTTTCACT	4076
300	TAGAATTCAA	TTCAAATTCT	TAATTCAAAT	TTAATTTTAA	GATTTCTTAA	4126

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301	AATGTTTTTTT	AAAAAAATG	CAAATCTCAT	TTTAAAGAGA	TGAAAGCAGA	4176
302	GTAAGTGGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
303	GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
304	CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
305	ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGGAAAT	4376
306	ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
307	AGTCAGGAGT	GTATTCTAAT	AAGTGTGCT	TATCTCTTAT	TTTCTTCTAC	4476
308	AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
309	TTTTTTCCCC	TTCATTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTTGA	4576
310	TTTTGTTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
311	GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
312	AATAAAAGTT	TGACTTGCAT	AC			4698
313						
314						
315						

--> 330 (2) INFORMATION FOR SEQ ID NO: 7:  
331 (i) SEQUENCE CHARACTERISTICS: 2419 shown (next page)  
--> 332 (A) LENGTH: 2418 base pairs  
333 (B) TYPE: nucleic acid  
334 (D) TOPOLOGY: linear  
335 (ii) MOLECULE TYPE: genomic DNA  
--> 336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

same  
STRANDEDNESS  
known, too

337						
338						
339	GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
340	GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
341	TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCCTGAG	150
342	GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
343	TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
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359	GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCCTGA	1050
360	GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
361	TGAAGGAAGC	AGACCCACAC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
362	GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
363	AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
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365	GGGAGGGAGC	ACAGTGCCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
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(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5724 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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395 (D) TOPOLOGY: linear
396 (ii) MOLECULE TYPE: genomic DNA
397 (ix) FEATURE:
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--> 399 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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(B) TYPE: nucleic acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: genomic DNA  
(ix) FEATURE:  
(A) NAME/KEY: MAGE-2 gene  
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606	GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
607	ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
608	GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
609	TTG AGA GAG	GGA GAA GAG	TGA			3542
610	GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
611	GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	TGTGATATGA	3642
612	GGCCCATTC	TGCCTCTTTG	AAGAGAGCAG	TCAGCATTC	TAGCAGTGAG	3692
613	TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
614	TTGTTCAAAT	GTTCCTTTTA	ACAAATGGTT	GGATGAACTT	CAGCATCCAA	3792
615	GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
616	TAAGAGTCCT	GTTTTTTTAT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892
617	TTGTACACATA	ATAACAGCAG	TGGAATATGT	ATTTGCCAT	ATTGTGAACG	3942
618	AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
619	TGCCTTATAC	CTCAGTCTAT	TATGTAAAAAT	TAAAAATATG	TGTATGTTTT	4042
620	TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
621	TCACTGGCTC	ATTTCTTTAC	CATTCACCTCA	GCATCTGCTC	TGTGGAAGGC	4142
622	CCTGGTAGTA	GTGGG				4157
623						
624						
625						
626						

627 (2) INFORMATION FOR SEQ ID NO: 10:

628 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:46

INPUT SET: S32279.raw

629 (A) LENGTH: 662 base pairs  
630 (B) TYPE: nucleic acid  
631 (D) TOPOLOGY: linear  
632 (ii) MOLECULE TYPE: genomic DNA  
633 (ix) FEATURE:  
634 (A) NAME/KEY: MAGE-21 gene  
--> 635 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
636  
637  
638  
639 GGATCCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC 50  
640 AGGGAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT 100  
641 CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG 150  
642 GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG 200  
643 ACTGAGGCGG GCCTCACCCC AGACAGAGGG CCCCAATAA TCCAGCGCTG 250  
644 CCTCTGCTGC CAGGCCTGGA CCACCCTGCA GGGGAAGACT TCTCAGGCTC 300  
645 AGTCGCCACC ACCTCACCCC GCCACCCCCC GCCGCTTTAA CCGCAGGGAA 350  
646 CTCTGGTGTA AGAGCTTTGT GTGACCAGGG CAGGGCTGGT TAGAAGTGCT 400  
647 CAGGGCCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCA AGAGGGGACT 450  
648 GAGGGTAACC CCCCCGCACC CCCACCACCA TTCCCATCCC CCAACACCAA 500  
649 CCCCACCCCC ATCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA 550  
650 ACGGCACCCC CAAACCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG 600  
651 GAGCTTTGCC CCTGCAATCA ACCCACGGAA GCTCCGGGAA TGGCGGCCAA 650  
652 GCACGCGGAT CC 662  
653  
654  
655

656 (2) INFORMATION FOR SEQ ID NO: 11:  
657 (i) SEQUENCE CHARACTERISTICS:  
658 (A) LENGTH: 1640 base pairs  
659 (B) TYPE: nucleic acid  
660 (D) TOPOLOGY: linear  
661 (ii) MOLECULE TYPE: cDNA to mRNA  
662 (ix) FEATURE:  
663 (A) NAME/KEY: cDNA MAGE-3  
--> 664 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
665  
666  
667 GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG 50  
668 GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA 100  
669 AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCCAC ACTCCCGCCT 150  
670 GTTGCCCTGA CCAGAGTCAT C 171  
671 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 213  
672 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 255  
673 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 297  
674 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339  
675 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381  
676 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423  
677 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465  
678 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507  
679 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549  
680 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:46

INPUT SET: S32279.raw

681	GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
682	TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
683	GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
684	GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
685	CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
686	AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
687	CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
688	TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
689	GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
690	GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
691	ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
692	GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
693	TTG AGA GAG GGG GAA GAG TGA	1116
694	GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
695	GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCCTCC TGTGACGTGA	1216
696	GGCCCATTC TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
697	TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
698	TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
699	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	1416
700	TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA	1466
701	TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	1516
702	GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
703	ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
704	ACCAGGATTT CCTTGACTTC TTTG	1640
705		
706		
707		
708		

709 (2) INFORMATION FOR SEQ ID NO: 12:  
710 (i) SEQUENCE CHARACTERISTICS:  
711 (A) LENGTH: 943 base pairs  
712 (B) TYPE: nucleic acid  
713 (D) TOPOLOGY: linear  
714 (ii) MOLECULE TYPE: genomic DNA  
715 (ix) FEATURE:  
716 (A) NAME/KEY: MAGE-31 gene  
--> 717 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

718		
719		
720	GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT	50
721	CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG	100
722	GCCCGTGGAT TCCTCTCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG	150
723	AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA	200
724	GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC	250
725	CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT	300
726	TTCACTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC	350
727	CTCTCACTTC CTCCTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC	400
728	AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG	450
729	TTAGAGCCTC CAAGGTTCCTC TTCAGTACTC AGCTGAGGTC TCTCACATGC	500
730	TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCACA	550
731	CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580
732	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	622

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999  
TIME: 16:48:47

INPUT SET: S32279.raw

733	GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG	664
734	CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	706
735	TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	748
736	GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	790
737	CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	832
738	GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	874
739	CCT GAC CTG GAG TCT GAG TTC CAA GCA CTC AGT AGG AAG	916
740	GTG GCC AAG TTG GTT CAT TTT CTG CTC	943
741		
742		
743		
744		

745 (2) INFORMATION FOR SEQ ID NO: 13:  
 746 (i) SEQUENCE CHARACTERISTICS:  
 747 (A) LENGTH: 2531 base pairs  
 748 (B) TYPE: nucleic acid  
 749 (D) TOPOLOGY: linear  
 750 (ii) MOLECULE TYPE: genomic DNA  
 751 (ix) FEATURE:  
 752 (A) NAME/KEY: *same* *MAGE-4 gene*  
 --> 753 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

754		
755		
756	GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
757	GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
758	TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG	150
759	GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
760	TGGTCTGAGA CAGTGTCTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
761	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
762	CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
763	CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA	400
764	CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
765	TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500
766	TAGAGCCTCT AAGATTGCT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550
767	TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTG	600
768	CCTGCTGCCC TGACCAGAGT CATC	624
769	ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
770	GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA	708
771	CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC	750
772	TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
773	GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
774	GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
775	AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918
776	TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
777	AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
778	GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044
779	ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
780	GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
781	GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
782	CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
783	TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
784	GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296



RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:47

INPUT SET: S32279.raw

785	GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
786	GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
787	CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
788	CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
789	GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
790	AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
791	GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
792	GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC	1628
793	ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC	1678
794	CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT	1728
795	TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT	1778
796	GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
797	TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
798	AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG	1928
799	GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT	1978
800	GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCTGCC TTATGCCCTCA	2028
801	GTCTATTCTG TAAAATTAA AAATATATAT GCATACCTGG ATTTCTTGG	2078
802	CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA	2128
803	ACTGGCTCAT TTCTTCTCTA TGCACGTGAGC ATCTGCTCTG TGGAAGGCC	2178
804	AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
805	GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT	2278
806	CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
807	GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA	2378
808	AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC	2428
809	AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC	2478
810	TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
811	GGG	2531
812		
813		
814		
815		

816 (2) INFORMATION FOR SEQ ID NO: 14:  
817 (i) SEQUENCE CHARACTERISTICS:  
818 (A) LENGTH: 2531 base pairs  
819 (B) TYPE: nucleic acid  
820 (D) TOPOLOGY: linear  
821 (ii) MOLECULE TYPE: genomic DNA  
822 (ix) FEATURE:  
823 (A) NAME/KEY: MAGE-41 gene  
--> 824 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

825		
826		
827	GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
828	GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
829	TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG	150
830	GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
831	TGGTCTGAGA CAGTGTCCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
832	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
833	CAAGACACAT AGGACTCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
834	CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA	400
835	CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
836	TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999

TIME: 16:48:47

INPUT SET: S32279.raw

837	TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550
838	TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTTG	600
839	CCTGCTGCCC TGAGCAGAGT CATC	624
840	ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
841	GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG	708
842	CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC	750
843	TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
844	GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
845	GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
846	AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918
847	TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
848	AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
849	GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044
850	ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
851	GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
852	GAA TCG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
853	CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
854	TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
855	GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296
856	GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
857	GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
858	CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
859	CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
860	GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
861	AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
862	GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
863	GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC	1628
864	ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC	1678
865	CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT	1728
866	TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT	1778
867	GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
868	TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
869	AGTCTTGTTT TTTATTTCAGA TTGGGAAATC CGTTCATTTT TGTGAATTTG	1928
870	GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT	1978
871	GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCTGCGC TTATGCCTCA	2028
872	GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCCTGG	2078
873	CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA	2128
874	ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCC	2178
875	AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
876	GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT	2278
877	CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
878	GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA	2378
879	AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC	2428
880	AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC	2478
881	TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
882	GGG	2531
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884		
885		

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886 (2) INFORMATION FOR SEQ ID NO: 15:  
887 (i) SEQUENCE CHARACTERISTICS:  
888 (A) LENGTH: 1068 base pairs

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:48

INPUT SET: S32279.raw

889 (B) TYPE: nucleic acid  
890 (D) TOPOLOGY: linear  
891 (ii) MOLECULE TYPE: cdna to mRNA  
892 (ix) FEATURE:  
893 (A) NAME/KEY: cdna MAGE-4  
894 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

--> 895  
896  
897  
898 G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 40  
899 GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 82  
900 CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 124  
901 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 166  
902 GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 208  
903 GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC 250  
904 ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 292  
905 GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 334  
906 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 376  
907 GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 418  
908 GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 460  
909 ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 502  
910 GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT 544  
911 CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG 586  
912 CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA 628  
913 TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC 670  
914 TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG 720  
915 TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG 770  
916 GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG 820  
917 GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA 870  
918 ATTTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA 920  
919 AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT 970  
920 AAGAGTCTTG TTTTATTTC AGATTGGGAA ATCCGTCTA TTTTGTAAT 1020  
921 TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC 1068  
922  
923  
924  
925

926 (2) INFORMATION FOR SEQ ID NO: 16:  
927 (i) SEQUENCE CHARACTERISTICS:  
928 (A) LENGTH: 2226 base pairs  
929 (B) TYPE: nucleic acid  
930 (D) TOPOLOGY: linear  
931 (ii) MOLECULE TYPE: genomic DNA  
932 (ix) FEATURE:  
933 (A) NAME/KEY: MAGE-5 gene  
934 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

--> 935  
936  
937 GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50  
938 GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC 100  
939 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150  
940 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT 200

*None even*  
*(see next page, too)*

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999  
TIME: 16:48:48

INPUT SET: S32279.raw

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941 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
942 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
943 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
944 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT 400
945 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
946 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
947 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTTCACT TTTTAGCTGA 550
948 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCC 600
949 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
--> 950 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA/ 684 686
--> 951 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTC CTG CTG 728 OK
952 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 770
953 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 812
954 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 854
955 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 896
956 TGG CTG ACT TGA 908
957 TTCAATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA 958
958 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCTTGAGAT 1008
959 CTTGCGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA 1058
960 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1108
961 CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG 1158
962 GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC 1208
963 CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG 1258
964 GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT 1308
965 TGGTGCAGGA AAACCTACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC 1358
966 ATATGCTATG AGTTACTGTG GGTCCAAGG GCACTCGCTG CTTGAAAAGTA 1408
967 CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATT TCTACCCATC 1458
968 CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG 1508
969 CTGCAGCCAG GGCCACTGCG AGGGGGGGCTG GGCCAGTGCA CCTTCCAGGG 1558
970 CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC 1608
971 TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT TCTGTTCTAT 1658
972 TGGATGACTT TGAGATTTGT CTTTGTTCCT TTTTGGAAAT GTTCAAATGT 1708
973 TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA 1758
974 CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT 1808
975 TTTTATTTC GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT 1858
976 TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAC 1908
977 TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC 1958
978 TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCCTTGGC 2008
979 TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT 2058
980 TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTGCTC TGTGGAAGGC 2108
981 CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA 2158
982 CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT 2208
983 GCCCTCTAAG ATGTAGAG 2226
984
985
986

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987 (2) INFORMATION FOR SEQ ID NO: 17:
988 (i) SEQUENCE CHARACTERISTICS:
989 (A) LENGTH: 2305 base pairs
990 (B) TYPE: nucleic acid
991 (D) TOPOLOGY: linear
992 (ii) MOLECULE TYPE: genomic DNA

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*same  
even  
(STRANDEDNESS)*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:48

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993 (ix) FEATURE:  
994 (A) NAME/KEY: MAGE-51 gene  
--> 995 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
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997  
998  
999 GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50  
1000 GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC 100  
1001 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150  
1002 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAACAGAC ACTGAGGCCT 200  
1003 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250  
1004 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300  
1005 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350  
1006 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCCT GAGGTGCCCT 400  
1007 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450  
1008 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500  
1009 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTTCACT TTTAGCTGA 550  
1010 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCACTGGGTC TCCATTGCCC 600  
1011 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644  
1012 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 686  
1013 GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC 728  
1014 AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT 770  
1015 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 812  
1016 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 854  
1017 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 896  
1018 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 938  
1019 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 980  
1020 TGG CTG ACT TGA 992  
1021 TTCATTTTCT GTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA 1042  
1022 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1092  
1023 CTTCCGGCAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA 1142  
1024 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCCTGGGA 1192  
1025 CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCCA GACGGGCCTC 1242  
1026 CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA 1292  
1027 GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG 1342  
1028 AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG 1392  
1029 CAGGAAAAC TACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC 1442  
1030 TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG 1492  
1031 CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCCTACC CATCCCTGCA 1542  
1032 TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG 1592  
1033 CCAGGGCCAC TGGGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT 1642  
1034 CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCAT TTTCTCTCTT 1692  
1035 TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTCCTGTT CTATTGGATG 1742  
1036 ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCCCTT 1792  
1037 TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG 1842  
1038 TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTAA 1892  
1039 TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC 1942  
1040 AGTGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAAGTATGTA 1992  
1041 GATAAGAAA TTAAAAGATA TTTAATCTT GCCTTATACT CAGTCTATTC 2042  
1042 GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT 2092  
1043 TGAGAAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT 2142  
1044 GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG 2192  
1045 GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCAGAGGG 2242

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
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1046	TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT	2292
1047	CTAAGATGTA GAG	2305
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1049		
1050		
1051		

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1052 (2) INFORMATION FOR SEQ ID NO: 18:  
1053 (i) SEQUENCE CHARACTERISTICS:  
1054 (A) LENGTH: 225 base pairs  
1055 (B) TYPE: nucleic acid  
1056 (D) TOPOLOGY: linear  
1057 (ii) MOLECULE TYPE: cDNA  
1058 (ix) FEATURE:  
1059 (A) NAME/KEY: MAGE-6 gene  
--> 1060 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
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1062

1063	TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG	42
1064	CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC	84
1065	GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC	126
1066	GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC	168
1067	TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC	210
1068	TGT GCC CCT GAG GAG	225
1069		
1070		
1071		
1072		

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1073 (2) INFORMATION FOR SEQ ID NO: 19:  
1074 (i) SEQUENCE CHARACTERISTICS:  
1075 (A) LENGTH: 1947 base pairs  
1076 (B) TYPE: nucleic acid  
1077 (D) TOPOLOGY: linear  
1078 (ii) MOLECULE TYPE: genomic DNA  
1079 (ix) FEATURE:  
1080 (A) NAME/KEY: MAGE-7 gene  
--> 1081 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
1082  
1083

1084	TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGAATCCAGA	50
1085	GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC	100
1086	TGGCCGGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA	150
1087	GCGGACAGGC CGGCCAGGAG GTCAGAAAGCC CCAGGAGGCC CCAGAGGAGC	200
1088	ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT	250
1089	GTTTCACAAA TGAGGCCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG	300
1090	GTTCCTCCCC ATCGCCCAGC TGCTGCCC GC ACTCCAGCCT GCTGCCCTGA	350
1091	CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG	400
1092	GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCTGGT GGGTGCGCAG	450
1093	GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA	500
1094	AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCAGT CCTCCCCTGA	550
1095	GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA	600
1096	GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC	650

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
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1097	TAGACACACC CCGCTCACCT GCGTCCTTG TTCCA	685
1098	ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT	727
1099	ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA	769
1100	GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT	811
1101	GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC	853
1102	ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA	895
1103	CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC	937
1104	AGA GCA TGC CCG AGA CCG GCC TTC TGA	964
1105	TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG	1014
1106	GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT	1064
1107	TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC	1114
1108	TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT	1164
1109	CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG	1214
1110	AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCTTA CCCATCCCCTG	1264
1111	CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC	1314
1112	AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTT	1364
1113	CACACATCCA CCACCTTCCC TGTCCTGTGA CATGAGGCC ATTCTTCACT	1414
1114	CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGG AGTGTGTTGG	1464
1115	GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC	1514
1116	GATTTGGAGG TTTATCTTTG TTTCTTTTGT CAGTCGTTCA AATGTTCTCT	1564
1117	TTAATGGATG GTGTAATGAA CTTCAACATT CATTTTCATGT ATGACAGTAG	1614
1118	GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT	1664
1119	TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG	1714
1120	CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAATATGG	1764
1121	GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG	1814
1122	CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA	1864
1123	GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA	1914
1124	AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG	1947
1125		
1126		
1127		

1128 (2) INFORMATION FOR SEQ ID NO: 20:  
1129 (i) SEQUENCE CHARACTERISTICS:  
1130 (A) LENGTH: 1810 base pairs  
1131 (B) TYPE: nucleic acid  
1132 (D) TOPOLOGY: linear  
1133 (ii) MOLECULE TYPE: genomic DNA  
1134 (ix) FEATURE:  
1135 (A) NAME/KEY: MAG-8 gene  
--> 1136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
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1138

1139	GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA	50
1140	TCACAGAGCA TAAGAGGCCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT	100
1141	GTTTCCCCTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA	150
1142	ACCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG	200
1143	GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA	250
1144	GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA	300
1145	CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA	350
1146	CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT	400
1147	CAATTGCCCA GCTCCGGCCC AACTCTCTCT GCTGCCCTGA CCTGAGTCAT	450
1148	C	451

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
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1149	• ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA	493
1150	GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG	535
1151	CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC	577
1152	TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT	619
1153	GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT	661
1154	TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT	703
1155	GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC	745
1156	CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT	787
1157	GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA	829
1158	TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG	871
1159	AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC	913
1160	AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT	955
1161	GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC	997
1162	ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT	1039
1163	CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC	1081
1164	ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC	1123
1165	TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA	1156
1166	TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG	1206
1167	AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT	1256
1168	CCTGTGCGCT ACGAGTTCCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG	1306
1169	CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA	1356
1170	TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT	1406
1171	TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG	1456
1172	GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCCT GCTCTGTTAC	1506
1173	ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA	1556
1174	GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC	1606
1175	AGTTCCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG	1656
1176	AATTGTTCCA ATGTTCCCTC TAATGGATGG TGTAATGAAC TTCAACATTC	1706
1177	ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA	1756
1178	GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA	1806
1179	ATTC	1810
1180		
1181		
1182		

1183 (2) INFORMATION FOR SEQ ID NO: 21:  
1184 (i) SEQUENCE CHARACTERISTICS:  
1185 (A) LENGTH: 1412 base pairs  
1186 (B) TYPE: nucleic acid  
1187 (D) TOPOLOGY: linear  
1188 (ii) MOLECULE TYPE: genomic DNA  
1189 (ix) FEATURE:  
1190 (A) NAME/KEY: MAGE-9 gene  
--> 1191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
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1193

1194	TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC	50
1195	AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT	100
1196	GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG	150
1197	TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC	200
1198	TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA	250
1199	GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT	300
1200	TGTTAGAACC TCCAAGGTTT GGTTCCTCAG TGAAGTCTCT CACACACTCC	350



RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:50

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1201	CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCAGCGTC	400
1202	CTGACTGCTG CCCTGACCAG AGTCATC	427
1203	ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA	469
1204	GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA	511
1205	CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT	553
1206	GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT	595
1207	CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC	637
1208	GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC	679
1209	AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT	721
1210	CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG	763
1211	GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG	805
1212	GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA	847
1213	AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC	889
1214	GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG	931
1215	GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC	973
1216	CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC	1015
1217	AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC	1057
1218	AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG	1099
1219	AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC	1141
1220	GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA	1183
1221	AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG	1225
1222	CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC	1267
1223	AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA	1309
1224	AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG	1351
1225	GGA GAG GAG CAA GAG GGA GTC TGA	1375
1226	GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA	1412
1227		
1228		
1229		

1230 (2) INFORMATION FOR SEQ ID NO: 22:  
1231 (i) SEQUENCE CHARACTERISTICS:  
1232 (A) LENGTH: 920 base pairs  
1233 (B) TYPE: nucleic acid  
1234 (D) TOPOLOGY: linear  
1235 (ii) MOLECULE TYPE: genomic DNA  
1236 (ix) FEATURE:  
1237 (A) NAME/KEY: MAGE-10 gene  
--> 1238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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1240		
1241	ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC ACCTACCCTA	50
1242	CTGTCACTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT	100
1243	CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA	150
1244	AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT	200
1245	GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA	250
1246	CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC	300
1247	ACACTCCAC CTGCTACCCT GATCAGAGTC ATC	333
1248	ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA	375
1249	GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA	417
1250	CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT	459
1251	TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC	501
1252	TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC	543

RAW SEQUENCE LISTING  
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1253	CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC	585
1254	CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT	627
1255	TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA	669
1256	AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT	711
1257	GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT	753
1258	TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG	795
1259	ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT	837
1260	GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC	879
1261	ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC	920
1262		
1263		
1264		
1265		

1266 (2) INFORMATION FOR SEQ ID NO: 23:  
1267 (i) SEQUENCE CHARACTERISTICS:  
1268 (A) LENGTH: 1107 base pairs  
1269 (B) TYPE: nucleic acid  
1270 (D) TOPOLOGY: linear  
1271 (ii) MOLECULE TYPE: genomic DNA  
1272 (ix) FEATURE:  
1273 (A) NAME/KEY: MAGE-11 gene  
--> 1274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

1275  
1276  
1277 AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT 50  
1278 CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT 100  
1279 CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG 150  
1280 GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG 200  
1281 AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG 250  
1282 CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC 300  
1283 AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTTACTCT GAATGTGGGC 350  
1284 ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC 400  
1285 TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC 450  
1286 TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG 500  
1287 CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA 550  
1288 GATAATTGAT TTGGTTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT 600  
1289 GATCACAAAAG GCAGAA 616  
1290 ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT 658  
1291 GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT 700  
1292 GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT 742  
1293 GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG 784  
1294 TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA 826  
1295 GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA 868  
1296 GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT 910  
1297 GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT 952  
1298 ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG 994  
1299 GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT 1036  
1300 CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG 1078  
1301 TAC ATA GCC AAT GCC AAT GGG AGG GAT CC 1107  
1302  
1303  
1304

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1305 (2) INFORMATION FOR SEQ ID NO: 24:  
1306 (i) SEQUENCE CHARACTERISTICS:  
1307 (A) LENGTH: 2150 base pairs  
1308 (B) TYPE: nucleic acid  
1309 (D) TOPOLOGY: linear  
1310 (ii) MOLECULE TYPE: genomic DNA  
1311 (ix) FEATURE:  
1312 (A) NAME/KEY: smage-I  
--> 1313 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
1314  
1315  
1316  
1317 TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT 50  
1318 CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC 100  
1319 ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC 150  
1320 TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT 200  
1321 GCCCTTGATAT GCAGGCCTAA GTTTTCTCTGT CTGCTTAACC CCTCCAAGTG 250  
1322 AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT 300  
1323 ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG 350  
1324 AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCTTAG AAAG 394  
1325 ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT 436  
1326 CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT 478  
1327 TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT 520  
--> 1328 AGT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG 565  
--> 1329 AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG 6040K  
1330 GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT 646  
1331 TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT 688  
1332 TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA 730  
1333 GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT 772  
1334 GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA 814  
1335 GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG 856  
1336 AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG 898  
1337 ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT 940  
1338 AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA 982  
1339 ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG 1024  
1340 GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA 1066  
1341 CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG 1108  
1342 TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC 1150  
1343 TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA 1192  
1344 TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG 1234  
1345 ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CCG 1276  
--> 1346 GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC 1314  
--> 1347 CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA 1360K  
1348 ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT 1402  
1349 GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT 1444  
1350 CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA 1486  
1351 GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT 1528  
1352 AAC ATG TAG 1537  
1353 TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG 1587  
1354 AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCTGTAT 1637  
1355 ACATTAGTAG AATGGAGGCT ATTTTGTGTTA CTTTTCAAAT GTTTGTTTAA 1687  
1356 CTAACACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC 1737

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PATENT APPLICATION US/08/819,669CDATE: 06/19/1999  
TIME: 16:48:51

INPUT SET: S32279.raw

1357	TGTCACCTTGT	CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
1358	ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
1359	GATTGTGATG	GCAATGTGAT	ATCATACAGT	GGTGAAACAA	CAGTGAAGTG	1887
1360	GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
1361	TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
1362	GACTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
1363	TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
1364	GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
1365	GTTATCAGAG	TCT				2150
1366						
1367						
1368						

1369 (2) INFORMATION FOR SEQ ID NO: 25:  
1370 (i) SEQUENCE CHARACTERISTICS:  
1371 (A) LENGTH: 2099 base pairs  
1372 (B) TYPE: nucleic acid  
1373 (D) TOPOLOGY: linear  
1374 (ii) MOLECULE TYPE: genomic DNA  
1375 (ix) FEATURE:  
1376 (A) NAME/KEY: smage-II  
--> 1377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

*STRANDEDNESS  
error*

1378						
1379						
1380	ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
1381	AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
1382	TTTGTCATGG	CACAGGTTTC	TGCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
1383	CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
1384	TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
1385	CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
1386	ACTAGACTTT	TATGCAGTGG	CCTAACAAGT	TTTAATTTCT	TCCACAGGGT	350
1387	TTGCAGAAAA	GAGCTTGATC	CACGAGTTTC	GAAGTCTTGG	TATGTTCCCTA	400
1388	GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
1389	AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
1390	TCTTTCCAGA	TTCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
1391	TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
1392	CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCACTG	CAGAGGAAGC	650
1393	AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
1394	CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
1395	TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
1396	AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTGAG	CACACACTGA	850
1397	AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
1398	AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
1399	TAACAAGAAG	TATAAGGAGC	AATTCCTTGA	GATCCTCAGG	AGAACTTCTG	1000
1400	CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
1401	ACTCATTCCT	ATTTGCTGGT	AGGCAAACCTG	GGTCTTTCCA	CTGAGGGAAG	1100
1402	TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAC	AGGTCTCCTA	ATGTCTGTCC	1150
1403	TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
1404	CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
1405	TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
1406	AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCCCTGTGG	1350
1407	GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTT	1400
1408	AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450

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1409	TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
1410	AAGGGTGTTT	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
1411	GAGTCTGTTC	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
1412	AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
1413	ATTAGTAGAA	TGGAGGCTAT	TTTTGTACT	TTTCAAATGT	TTGTTTAACT	1700
1414	AAACAGTGCT	TTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAAGTG	1750
1415	TCACTTGTC	GATTAGGACT	TGTTTTGTGA	TTTGCAACAA	ACTGGAAAAC	1800
1416	ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
1417	TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
1418	AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
1419	CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTTGATGA	2000
1420	CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACTCTA	TTACTTTATT	2050
1421	ATTTTCTTCA	ATTATTAATT	AAGCATTTGGT	TATCTGGAAG	TTTCTCCAG	2099
1422						
1423						
1424						
1425						

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# SEQUENCE VERIFICATION REPORT

## PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999

TIME: 16:48:52

INPUT SET: S32279.raw

Line	Error	Original Text
30	Wrong Classification	(C) CLASSIFICATION: 435
73	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
96	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
152	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
168	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
212	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
332	Entered (2418) and Calc. Seq. Length (2419) differ	(A) LENGTH: 2418 base pairs
336	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
387	# of Sequences for line conflicts w/ running total	AATGATCTTG GGTGGATCC
393	Entered (5724) and Calc. Seq. Length (5674) differ	(A) LENGTH: 5724 base pairs
399	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
463	# of Sequences for line conflicts w/ running total	GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACC
531	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
635	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
664	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
717	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
753	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
824	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
894	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
934	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
950	# of Sequences for line conflicts w/ running total	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC A
951	# of Sequences for line conflicts w/ running total	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG T
995	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
1060	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
1081	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
1136	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
1191	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
1238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
1274	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
1313	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
1328	# of Sequences for line conflicts w/ running total	ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT A
1329	# of Sequences for line conflicts w/ running total	AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG C
1346	# of Sequences for line conflicts w/ running total	GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT G
1347	# of Sequences for line conflicts w/ running total	CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA G
1377	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25: